

What is claimed is:

1. A method comprising comparing an expression profile of at least one gene in a peripheral blood sample of a patient to a reference expression profile of said at least one gene, wherein said at least one gene is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients who have a non-blood disease and are subject to a drug therapy as compared to PBMCs isolated from said patients before said drug therapy, and wherein the patient has the non-blood disease and is being treated by said drug therapy.
2. The method according to claim 1, wherein said drug therapy is a CCI-779 therapy.
3. The method according to claim 2, wherein the non-blood disease is a solid tumor.
4. The method according to claim 3, wherein the solid tumor is RCC.
5. The method according to claim 2, wherein said at least one gene includes one or more genes selected from Table 5.
6. The method according to claim 2, wherein said at least one gene includes at least two genes selected from Table 5.
7. The method according to claim 1, wherein the peripheral blood sample is a whole blood sample.
8. The method according to claim 1, wherein the peripheral blood sample comprises enriched PBMCs.
9. The method according to claim 1, wherein the expression profile is determined by RT-PCR or immunoassays.

10. The method according to claim 1, wherein the reference expression profile is an average expression profile of said at least one gene in peripheral blood samples isolated from said patients before said drug therapy.

11. The method according to claim 1, wherein the reference expression profile is an expression profile of said at least one gene in a reference peripheral blood sample isolated from the patient before said drug therapy.

12. The method according to claim 1, wherein said at least one gene includes one or more genes which are over-expressed or under-expressed in PBMCs of patients who have the non-blood disease as compared to PBMCs of humans who do not have the non-blood disease, and wherein said drug therapy is capable of down-regulating or up-regulating expression of said one or more genes in PBMCs of patients who have the non-blood disease.

13. The method according to claim 1, wherein said at least one gene includes one or more genes whose expression in PBMCs is capable of being increased or reduced by a phytohemagglutinin treatment, and wherein said drug therapy is capable of down-regulating or up-regulating expression of said one or more genes in phytohemagglutinin-treated PBMCs.

14. The method according to claim 1, wherein RNA transcripts of said at least one gene are capable of hybridizing under stringent or nucleic acid array hybridization conditions to one or more qualifiers selected from the Qualifier Table.

15. The method according to claim 14, wherein said drug therapy is a CCI-779 therapy.

16. The method according to claim 15, wherein the non-blood disease is RCC.

17. A method for identifying drug activity genes, comprising:  
detecting an expression profile of genes in peripheral blood samples of patients who have a non-blood disease and are subject to a drug therapy; and

comparing said expression profile to a baseline expression profile of said genes in peripheral blood samples isolated from said patients before said drug therapy so as to identify drug activity genes whose expression levels in peripheral blood samples can be modulated by said drug therapy.

18. A kit comprising a plurality of polynucleotides, wherein each of said polynucleotides is capable of hybridizing under stringent or nucleic acid array hybridization conditions to an RNA transcript, or the complement thereof, of a different respective gene selected from Table 5.

19. A kit comprising a plurality of antibodies, wherein each of said antibodies is capable of binding to a polypeptide encoded by a different respective gene selected from Table 5.

20. A nucleic acid array comprising polynucleotide probes, wherein a substantial portion of all polypeptide probes on the nucleic acid array can hybridize under stringent or nucleic acid array hybridization conditions to RNA transcripts, or the complements thereof, of genes selected from Table 5.